- Hierarchical clustering is a widely used data analysis tool.
- The idea is to build a binary tree of the data that successively merges similar groups of points
- Visualizing this tree provides a useful summary of the data

- Recall that k-means or k-medoids requires
 - A number of clusters k
 - An initial assignment of data to clusters
 - A distance measure between data $d(x_n, x_m)$
- Hierarchical clustering only requires a measure of similarity between *groups* of data points.

- We will talk about agglomerative clustering.
- Algorithm:
 - 1 Place each data point into its own singleton group
 - 2 Repeat: iteratively merge the two closest groups
 - **③** Until: all the data are merged into a single cluster



Data



iteration 001

V1

D. Blei Clustering 02



iteration 002

V1

D. Blei Clustering 02



iteration 003

V1

D. Blei Clustering 02



iteration 004

vi



iteration 005



iteration 006



iteration 007



iteration 008



iteration 009



iteration 010



iteration 011



iteration 012



iteration 013



iteration 014



iteration 015



iteration 016



iteration 017







V1



iteration 021

V1



iteration 022



iteration 023

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iteration 024

V1

- Each level of the resulting tree is a segmentation of the data
- The algorithm results in a sequence of groupings
- It is up to the user to choose a "natural" clustering from this sequence

- Agglomerative clustering is *monotonic*
 - The similarity between merged clusters is monotone decreasing with the level of the merge.
- *Dendrogram*: Plot each merge at the (negative) similarity between the two merged groups
- Provides an interpretable visualization of the algorithm and data
- Useful summarization tool, part of why hierarchical clustering is popular

Dendrogram of example data

Height 。 _ 851 1616 184 252 477 2641 2489 2278 22905 22905 2085 2085 2743 2743 2743 2425 024 455

Cluster Dendrogram



Groups that merge at high values relative to the merger values of their subgroups are candidates for natural clusters. (Tibshirani et al., 2001)

Group similarity

- Given a distance measure between points, the user has many choices for how to define intergroup similarity.
- Three most popular choices
 - Single-linkage: the similarity of the closest pair

$$d_{SL}(G,H) = \min_{i \in G, j \in H} d_{i,j}$$

• Complete linkage: the similarity of the furthest pair

$$d_{CL}(G,H) = \max_{i \in G, j \in H} d_{i,j}$$

• Group average: the average similarity between groups

$$d_{GA} = \frac{1}{N_G N_H} \sum_{i \in G} \sum_{j \in H} d_{i,j}$$

- Single linkage can produce "chaining," where a sequence of close observations in different groups cause early merges of those groups
- Complete linkage has the opposite problem. It might not merge close groups because of outlier members that are far apart.
- Group average represents a natural compromise, but depends on the scale of the similarities. Applying a monotone transformation to the similarities can change the results.

- Hierarchical clustering should be treated with caution.
- Different decisions about group similarities can lead to vastly different dendrograms.
- The algorithm *imposes* a hierarchical structure on the data, even data for which such structure is not appropriate.